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Application Serial Number: _10/589,594_

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Date Processed by STIC: _8/28/06_

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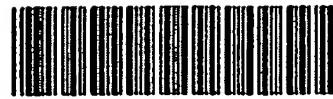   http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

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Revised 01/10/06

IFWP

RAW SEQUENCE LISTING   DATE: 08/28/2006
PATENT APPLICATION: US/10/589,594   TIME: 10:43:27

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        Output Set: N:\CRF4\08282006\J589594.raw

   4 <110> APPLICANT: Nakamura, Yusuke
   5   Furukawa, Yoichi
   7 <120> TITLE OF INVENTION: METHOD FOR DIAGNOSING COLORECTAL CANCERS
  10 <130> FILE REFERENCE: 082368-008900US
:--> 12 <140> CURRENT APPLICATION NUMBER: US/10/589,594
:--> 12 <141> CURRENT FILING DATE: 2006-08-15
  12 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/002145
  13 <151> PRIOR FILING DATE: 2004-02-24
  15 <160> NUMBER OF SEQ ID NOS: 23
  17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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  22 <213> ORGANISM: Homo sapiens
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  26 <222> LOCATION: (294)...(1688)
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  31 ggaccgccag ggagggcagg tcagtgggca gatcgcgtcc gcgggattca atctctgccc 180
  32 gctctgataa cagtcctttt ccctggcgct cacttcgtgc ctggcacccg gctgggcgcc 240
  33 tcaagaccgt tgtctcttcg atcgcttctt tggacttggc gaccatttca gag atg   296
  34   Met
  35   1
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  38 Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys
  39   5   10   15
  41 cct agt aac tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa 392
  42 Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu
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  45 att gca cac tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga 440
  46 Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly
  47   35   40   45
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  51 50   55   60   65
  53 ctt gag gct gag aag gag aag aat gct tat caa ctc aca gag aag gac 536
  54 Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys Asp
  55   70   75   80
  57 aaa gaa ata cag cga ctg aga gac caa ctg aag gcc aga tat agt act 584
  58 Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr
  59   85   90   95

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62 Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu Arg
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65 agg gag cag gtg ttg aaa gcc tta tct gaa gag aaa gac gta ttg aaa   680
66 Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu Lys
67     115             120             125
69 caa cag ttg tct gct gca acc tca cga att gct gaa ctt gaa agc aaa   728
70 Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser Lys
71 130             135             140             145
73 acc aat aca ctc cgt tta tca cag act gtg gct cca aac tgc ttc aac   776
74 Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe Asn
75         150             155             160
77 tca tca ata aat aat att cat gaa atg gaa ata cag ctg aaa gat gct   824
78 Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp Ala
79         165             170             175
81 ctg gag aaa aat cag cag tgg ctc gtg tat gat cag cag cgg gaa gtc   872
82 Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu Val
83         180             185             190
85 tat gta aaa gga ctt tta gca aag atc ttt gag ttg gaa aag aaa acg   920
86 Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys Thr
87     195             200             205
89 gaa aca gct gct cat tca ctc cca cag cag aca aaa aag cct gaa tca   968
90 Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu Ser
91 210             215             220             225
93 gaa ggt tat ctt caa gaa gag aag cag aaa tgt tac aac gat ctc ttg   1016
94 Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu Leu
95             230             235             240
97 gca agt gca aaa aaa gat ctt gag gtt gaa cga caa acc ata act cag   1064
98 Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr Gln
99         245             250             255
101 ctg agt ttt gaa ctg agt gaa ttt cga aga aaa tat gaa gaa acc caa   1112
102 Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr Gln
103         260             265             270
105 aaa gaa gtt cac aat tta aat cag ctg ttg tat tca caa aga agg gca   1160
106 Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg Ala
107     275             280             285
109 gat gtg caa cat ctg gaa gat gat agg cat aaa aca gag aag ata caa   1208
110 Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile Gln
111 290             295             300             305
113 aaa ctc agg gaa gag aat gat att gct agg gga aaa ctt gaa gaa gag   1256
114 Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu Glu
115             310             315             320
117 aag aag aga tcc gaa gag ctc tta tct cag gtc cag ttt ctt tac aca   1304
118 Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr Thr
119         325             330             335
121 tct ctg cta aag cag caa gaa gaa caa aca agg gta gct ctg ttg gaa   1352
122 Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu Glu
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130 Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu Arg
131 370                   375                   380                   385
133 aaa gca aga aat caa ata aca cag ttg gaa tcc ttg aaa cag ctt cat  1496
134 Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu His
135                   390                   395                   400
137 gag ttt gcc atc aca gag cca tta gtc act ttc caa gga gag act gaa  1544
138 Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr Glu
139                   405                   410                   415
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142 Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala Leu
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146 Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro Ala
147     435                   440                   445
149 act gag cat cgc gat ctg ctt gtc cat gtg gaa tac tgt tca aag tag  1688
150 Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys   *
151 450                   455                   460
153 caaaataagt atttgttttg atattaaaag attcaatact gtattttctg ttagcttgtg 1748
154 ggcattttga attatatatt tcacattttg cataaaactg cctatctacc tttgacactc 1808
155 cagcatgcta gtgaatcatg tatcttttag gctgctgtgc atttctcttg gcagtgatac 1868
156 ctccctgaca tggttcatca tcaggctgca atgacagaat gtggtgagca gcgtctactg 1928
157 agactactaa catttttgcac tgtcaaaata cttggtgagg aaaagatagc tcaggttatt 1988
158 gctaatgggt taatgcacca gcaagcaaaa tattttatgt tttgggggtt tgaaaaatca 2048
159 aagataatta accaaggatc ttaactgtgt tcgcattttt tatccaagca cttagaaaac 2108
160 ctacaatcct aattttgatg tccattgtta agaggtggtg atagatacta ttttttttt  2168
161 catattgtat agcggttatt agaaaagttg gggattttct tgatctttat tgctgcttac 2228
162 cattgaaact taacccagct gtgttcccca actctgttct gcgcacgaaa cagtatctgt 2288
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164 tgtaacttga attacattag cacattctgc ttagctaaaa ttgttaaaat aaactttaat 2408
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166 gctgggcaat gtaatgatca gatctttgtt tgtctgaaca ggtatttta tacatgcttt  2528
167 ttgtaaacca aaaactttta aatttcttca ggttttctaa catgcttacc actgggctac 2588
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173 <213> ORGANISM: Homo sapiens
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179                   20                  25                  30
180 Glu Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys
181             35                  40                  45
182 Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg
183     50                  55                  60
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185 65                  70                  75                  80
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187                  85                  90                  95
188 Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu
189                  100                 105                 110
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191          115                 120                 125
192 Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser
193      130                 135                 140
194 Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe
195 145                 150                 155                 160
196 Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp
197                  165                 170                 175
198 Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu
199                  180                 185                 190
200 Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys
201          195                 200                 205
202 Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu
203      210                 215                 220
204 Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu
205 225                 230                 235                 240
206 Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr
207                  245                 250                 255
208 Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr
209                  260                 265                 270
210 Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg
211          275                 280                 285
212 Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile
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214 Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu
215 305                 310                 315                 320
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217                  325                 330                 335
218 Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu
219                  340                 345                 350
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222 Asp Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu
223      370                 375                 380
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225 385                 390                 395                 400
226 His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr
227                  405                 410                 415
228 Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala
229                  420                 425                 430
230 Leu Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro
231                  435                 440                 445
232 Ala Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys
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RAW SEQUENCE LISTING   DATE: 08/28/2006
PATENT APPLICATION: US/10/589,594 .   TIME: 10:43:27

Input Set : A:\082368-008900US.txt
Output Set: N:\CRF4\08282006\J589594.raw

233   · 450   455   460
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242 <223> OTHER INFORMATION: An artificially synthesized primer sequence for
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297 <211> LENGTH: 27
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/28/2006
PATENT APPLICATION: US/10/589,594   TIME: 10:43:28

Input Set : A:\082368-008900US.txt
Output Set: N:\CRF4\08282006\J589594.raw

lease Note:
se of n and/or Xaa have been detected in the Sequence Listing. Please review the
equence Listing to ensure that a corresponding explanation is presented in the <220>
o <223> fields of each sequence which presents at least one n or Xaa.

eq#:23; N Pos. 489,490,491,492

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/589,594

DATE: 08/28/2006
TIME: 10:43:28

Input Set : A:\082368-008900US.txt
Output Set: N:\CRF4\08282006\J589594.raw

:12 M:270 C: Current Application Number differs, Replaced Current Application No
:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
:485 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
:489 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
:498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:480

<210> 23
<211> 5089
<212> DNA
<213> Artificial Sequence

<220>
<223> An artificially synthesized vector sequence

<221> misc_feature
<222> (489)...(492)
<223> n = GAP

"n" can only represent a single nucleotide, nothing else

<400> 23